

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/790,043

DATE: 03/13/97 #2

TIME: 10:20:52

INPUT SET: S16152.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information

(i) APPLICANT: Lonsdale, John
Milner, Peter
Payne, David
Pearson, Stewart

(ii) TITLE OF THE INVENTION: Novel FabI

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation
(B) STREET: 709 Swedeland Road
(C) CITY: King of Prussia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19406-0939

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 24-JAN-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/024845
(B) FILING DATE: 28-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Gimmi, Edward R
(B) REGISTRATION NUMBER: 38,891
(C) REFERENCE/DOCKET NUMBER: GM50005

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 610-270-4478

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47 (B) TELEFAX: 610-270-5090
48 (C) TELEX:
49
50

51 (2) INFORMATION FOR SEQ ID NO:1:
52

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 256 amino acids
55 (B) TYPE: amino acid
56 (C) STRANDEDNESS: single
57 (D) TOPOLOGY: linear
58

59 (ii) MOLECULE TYPE: protein
60

61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
62

63 Met Leu Asn Leu Glu Asn Lys Thr Tyr Val Ile Met Gly Ile Ala Asn
64 1 5 10 15
65 Lys Arg Ser Ile Ala Phe Gly Val Ala Lys Val Leu Asp Gln Leu Gly
66 20 25 30
67 Ala Lys Leu Val Phe Thr Tyr Arg Lys Glu Arg Ser Arg Lys Glu Leu
68 35 40 45
69 Glu Lys Leu Leu Glu Gln Leu Asn Gln Pro Glu Ala His Leu Tyr Gln
70 50 55 60
71 Ile Asp Val Gln Ser Asp Glu Glu Val Ile Asn Gly Phe Glu Gln Ile
72 65 70 75 80
73 Gly Lys Asp Val Gly Asn Ile Asp Gly Val Tyr His Ser Ile Ala Phe
74 85 90 95
75 Ala Asn Met Glu Asp Leu Arg Gly Arg Phe Ser Glu Thr Ser Arg Glu
76 100 105 110
77 Gly Phe Leu Leu Ala Gln Asp Ile Ser Ser Tyr Ser Leu Thr Ile Val
78 115 120 125
79 Ala His Glu Ala Lys Lys Leu Met Pro Glu Gly Gly Ser Ile Val Ala
80 130 135 140
81 Thr Thr Tyr Leu Gly Gly Glu Phe Ala Val Gln Asn Tyr Asn Val Met
82 145 150 155 160
83 Gly Val Ala Lys Ala Ser Leu Glu Ala Asn Val Lys Tyr Leu Ala Leu
84 165 170 175
85 Asp Leu Gly Pro Asp Asn Ile Arg Val Asn Ala Ile Ser Ala Gly Pro
86 180 185 190
87 Ile Arg Thr Leu Ser Ala Lys Gly Val Gly Gly Phe Asn Thr Ile Leu
88 195 200 205
89 Lys Glu Ile Glu Glu Arg Ala Pro Leu Lys Arg Asn Val Asp Gln Val
90 210 215 220
91 Glu Val Gly Lys Thr Ala Ala Tyr Leu Leu Ser Asp Leu Ser Ser Gly
92 225 230 235 240
93 Val Thr Gly Glu Asn Ile His Val Asp Ser Gly Phe His Ala Ile Lys
94 245 250 255
95

96 (2) INFORMATION FOR SEQ ID NO:2:
97

98 (i) SEQUENCE CHARACTERISTICS:

99 (A) LENGTH: 771 base pairs

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100 (B) TYPE: nucleic acid
101 (C) STRANDEDNESS: double
102 (D) TOPOLOGY: linear
103
104 (ii) MOLECULE TYPE: Genomic DNA
105
106 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
107
108 ATGTTAAATC TTGAAAACAA AACATATGTC ATCATGGGAA TCGCTAATAA GCGTAGTATT 60
109 GCTTTTGGTG TCGCTAAAGT TTTAGATCAA TTAGGTGCTA AATTAGTATT TACTTACCGT 120
110 AAAGAACGTA GCCGTAAAGA GCTTGAAAAA TTATTAGAAC AATTAAATCA ACCAGAAGCG 180
111 CACTTATATC AAATTGATGT TCAAAGCGAT GAAGAGGTTA TTAATGGTTT TGAGCAAATT 240
112 GGTAAGATG TTGGCAATAT TGATGGTGTA TATCATTCAA TCGCATTTGC TAATATGGAA 300
113 GACTTACGCG GACGCTTTTC TGAAACTTCA CGTGAAGGCT TCTTGTTAGC TCAAGACATT 360
114 AGTTCTTACT CATTAACAAT TGTGGCTCAT GAAGCTAAAA AATTAATGCC AGAAGGTGGT 420
115 AGCATTGTTG CAACAACATA TTTAGGTGGC GAATTCGCAG TTCAAAATTA TAATGTGATG 480
116 GGTGTTGCTA AAGCGAGCTT AGAAGCAAAT GTTAAATATT TAGCATTAGA CTTAGGTCCT 540
117 GATAATATTC GCGTTAATGC AATTTTCAGCT GGTCCAATCC GTACATTAAG TGCAAAAGGT 600
118 GTGGGTGGTT TCAATACAAT TCTTAAAGAA ATCGAAGAGC GTGCACCTTT AAAACGTAAC 660
119 GTTGATCAAG TAGAAGTAGG TAAAACAGCG GCTTACTTTR TAAGTGACTT ATCAAGTGGC 720
120 GTTACAGGTG AAAATATTCA TGTAGATAGC GGATTCCACG CAATTAAATA A 771

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SEQUENCE VERIFICATION REPORT

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Original Text